

## Claims

### Claims 1-19 (Canceled)

20. (Previously presented) A method for compensating for drift in fingerprint spectra due to differences in environmental factors that affect the metabolic state of microorganisms, comprising:

culturing under a first set of environmental factors a first microorganism and a second microorganism that is presumably metabolically similar to the first microorganism;

measuring a fingerprint spectrum of the first microorganism cultured under the first set of environmental factors and a fingerprint spectrum of the second microorganism cultured under the first set of environmental factors;

obtaining a fingerprint spectrum of the second microorganism cultured under a second set of environmental factors that differ from the first set of environmental factors and affect the metabolic state of the first and second microorganisms;

deriving a relationship between the fingerprint spectrum of the second microorganism cultured under the first set of environmental factors and the fingerprint spectrum of the second microorganism cultured under the second set of environmental factors; and,

applying the relationship derived for the second microorganism to transform the fingerprint spectrum of the first microorganism cultured under the first set of environmental factors to an expected fingerprint spectrum for the first microorganism under the second set of environmental factors that is compensated for drift due to the differences between the first and second sets of environmental factors that affect the metabolic state of the first microorganism.

21. (Currently amended) The method of claim 20, wherein culturing under a first set of environmental factors comprises culturing on a test growth medium and culturing under the second set of environmental factors comprises culturing on a library growth medium that differs from the test growth medium.

22. (Currently amended) The method of claim 20, wherein the fingerprint spectra are selected from the group consisting of mass spectra, electron impact mass spectra, pyrolysis mass

spectra, MAB mass spectra, MALDI mass spectra, ESI mass spectra, infrared spectra, Fourier-transform infrared spectra, diffuse reflectance infrared spectra, attenuated total reflectance infrared spectra, ion-mobility spectra, gas chromatograms, fatty-acid methyl ester gas chromatograms, liquid chromatograms, and nuclear magnetic resonance spectra, and portions and combinations thereof.

23. (Currently amended) The method of claim 20 further including a step of identifying the first microorganism by detecting a similarity between the expected fingerprint spectrum for the second microorganism and a fingerprint spectrum of a known organism cultured under the second set of environmental factors.

24. (Currently amended) The method of claim 23, wherein detecting a similarity is accomplished by a pattern recognition method selected from the group consisting of statistical pattern recognition methods, artificial intelligence pattern recognition methods, and combinations thereof.

25. (Currently amended) The method of claim 20, wherein the derived relationship comprises proportional differences in individual elements of the fingerprint spectra of the second microorganism between the first and second sets of environmental factors.

26. (Currently amended) The method of claim 20, wherein the first microorganism is presumed to be a bacterium belonging to a certain class of physiologically similar bacteria and the second, presumably metabolically similar microorganism belongs to the same class of physiologically similar bacteria, but the first and second microorganisms belong to different genera of bacteria of the same class of physiologically similar bacteria.

27. (Currently amended) The method of claim 20, wherein the first microorganism is presumed to be a bacterium belonging to a certain genus of bacteria and the second, presumably metabolically similar microorganism is of the same genus of bacteria, but the first and second microorganisms belong to different species of bacteria of the same genus of bacteria.

28. (Currently amended) The method of claim 20, wherein the first microorganism is presumed to be a bacterium belonging to a certain species of bacteria and the second, presumably metabolically similar microorganism is of the same species of bacteria, but the first and second microorganisms belong to different strains of the same species of bacteria.

29. (Currently amended) The method of claim 20, wherein the second, presumably metabolically similar microorganism is a representative of a metabolic similarity group that exhibits a fingerprint spectrum that is closest in canonical variate or principal component space to the fingerprint spectrum exhibited by the first microorganism under the first set of environmental conditions.

30. (Currently amended) The method of claim 29, wherein the second, presumably metabolically similar microorganism is a distance-weighted composite of two or more representatives of metabolic similarity groups.

31. (Currently amended) The method of claim 20, wherein the first set of environmental factors and the second set of environmental factors comprise the same batch of the same growth medium and the first set of environmental factors and the second set of environmental factors differ in at least one parameter selected from the group consisting of temperature, pressure, exposure to light, and exposure to gases.

32. (Currently amended) The method of claim 20, wherein the method is computer implemented.

Claims 33-66 (Canceled)

67. (Withdrawn, currently amended) The method of claim 20, wherein the first and second sets of environmental factors comprise different growth media.

68. (Withdrawn, currently amended) The method of claim 20, wherein the first and second sets of environmental factors comprise two batches of the same type of growth media.

69. (Currently amended) The method of claim 22, wherein the fingerprint spectra are pyrolysis mass spectra.

70. (Currently amended) The method of claim 20[[,]] further comprising adding the expected spectrum of the first microorganism to a database.

71. (Currently amended) The method of claim 31, wherein the first and second sets of environmental factors differ in temperature.

Claims 72-80 (Canceled).